<110> Falco, Saverio Carl
      Famodu, Layo
      Rafalski, Jan A.
      Ramaker, Michael
      Tarczynski, Mitchell C.
      Thorpe, Catherine

<120> PLANT METHIONINE SYNTHASE GENE AND METHODS FOR INCREASING THE
      METHIONINE CONTENT OF THE SEEDS OF PLANTS

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Asp Leu Glu Lys Val Ala Thr Asp Leu Arg Ser Ser Ile Trp Lys Gln
          35                  40                  45

Met Ser Glu Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Ser Ser Tyr
      50                  55                  60

Tyr Asp Gln Val Leu Asp Thr Thr Ala Met Leu Gly Ala Val Pro Glu
 65                  70                  75                  80

Arg Tyr Ser Trp Thr Gly Gly Glu Ile Gly Leu Ser Thr Tyr Phe Ser
              85                  90                  95

Met Ala Arg Gly Asn Ala Thr Val Pro Ala Met Glu Met Thr Lys Trp
             100                 105                 110

Phe Asp Thr Asn Tyr His Phe Ile Val Pro Glu Leu Gly Pro Ser Thr
             115                 120                 125

Lys Phe Thr Tyr Ala Ser His Lys Ala Val Ser Glu Tyr Lys Glu Ala
         130                 135                 140

Lys Ala Leu Gly Ile Asp Thr Val Pro Val Leu Val Gly Pro Val Ser
145                 150                 155                 160

Tyr Leu Leu Leu Ser Lys Pro Ala Lys Gly Val Glu Lys Ser Phe Ser
                 165                 170                 175

Leu Leu Ser Leu Leu Gly Ser Ile Leu Pro Ile Tyr Lys Glu Val Val
             180                 185                 190

Ala Glu Leu Lys Ala Ala Gly Ala Ser Trp Ile Gln Leu Asp Glu Pro
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2

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Thr Leu Val Lys Asp Leu Asp Ala His Glu Leu Ala Ala Phe Ser Ser
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Ala Tyr Ala Glu Leu Glu Ser Ser Phe Ser Gly Leu Asn Val Leu Ile
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Glu Thr Tyr Phe Ala Asp Ile Pro Ala Glu Ser Tyr Lys Thr Leu Thr
            245             250             255

Ser Leu Ser Gly Val Thr Ala Tyr Gly Phe Asp Leu Ile Arg Gly Ala
            260             265             270

Lys Thr Leu Asp Leu Ile Arg Ser Ser Phe Pro Ser Gly Lys Tyr Leu
        275             280             285

Phe Ala Gly Val Val Asp Gly Arg Asn Ile Trp Ala Asp Asp Leu Ala
    290             295             300

Ala Ser Leu Ser Thr Leu His Ser Leu Glu Ala Val Ala Gly Lys Asp
305             310             315                         320

Lys Leu Val Val Ser Thr Ser Cys Ser Leu Met His Thr Ala Val Asp
            325             330             335

Leu Val Asn Glu Thr Lys Leu Asp Asp Glu Ile Lys Ser Trp Leu Ala
        340             345             350

Phe Ala Ala Gln Lys Val Val Glu Val Asn Ala Leu Ala Lys Ala Leu
        355             360             365

Ala Gly Gln Lys Asp Glu Val Tyr Phe Ala Ala Asn Ala Ala Ala Gln
    370             375             380

Ala Ser Arg Arg Ser Ser Pro Arg Val Thr Asn Glu Glu Val Gln Lys
385             390             395                         400

Ala Ala Ala Ala Leu Arg Gly Ser Asp His Arg Arg Ser Thr Thr Val
            405             410             415

Ser Ala Arg Leu Asp Ala Gln Gln Lys Lys Leu Asn Leu Pro Val Leu
        420             425             430

Pro Thr Thr Thr Ile Gly Ser Phe Pro Gln Thr Val Glu Leu Arg Arg
    435             440             445

Val Arg Arg Glu Tyr Lys Ala Lys Lys Ile Thr Glu Asp Glu Tyr Ile
    450             455             460

Ser Ala Ile Lys Glu Glu Ile Ser Lys Val Val Lys Ile Gln Glu Glu
465             470             475                         480

Leu Asp Ile Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met
            485             490             495

Val Glu Tyr Phe Gly Glu Gln Leu Ser Gly Phe Ala Phe Thr Ala Asn
            500             505             510

Gly Trp Val Gln Ser Tyr Gly Ser Arg Cys Val Lys Pro Pro Ile Ile
        515             520             525
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3

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Tyr Gly Asp Val Ser Arg Pro Asn Pro Met Thr Val Phe Trp Ser Lys
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Met Ala Gln Ser Met Thr Pro Arg Pro Met Lys Gly Met Leu Thr Gly
545             550             555                 560

Pro Val Thr Ile Leu Asn Trp Ser Phe Val Arg Asn Asp Gln Pro Arg
                565             570             575

Phe Glu Thr Cys Tyr Gln Ile Ala Leu Ala Ile Lys Lys Glu Val Glu
            580             585             590

Asp Leu Glu Ala Ala Gly Ile Gln Val Ile Gln Ile Asp Glu Ala Ala
        595             600             605

Leu Arg Glu Gly Leu Pro Leu Arg Lys Ser Glu His Ala Phe Tyr Leu
    610             615             620

Asp Trp Ala Val His Ser Phe Arg Ile Thr Asn Cys Gly Val Gln Asp
625             630             635             640

Thr Thr Gln Ile His Thr His Met Cys Tyr Ser Asn Phe Asn Asp Ile
            645             650             655

Ile His Ser Ile Ile Asp Met Asp Ala Asp Val Ile Thr Ile Glu Asn
        660             665             670

Ser Arg Ser Asp Glu Lys Leu Leu Ser Val Phe Arg Glu Gly Val Lys
        675             680             685

Tyr Gly Ala Gly Ile Gly Pro Gly Val Tyr Asp Ile His Ser Pro Arg
    690             695             700

Ile Pro Ser Thr Glu Glu Ile Ala Asp Arg Val Glu Lys Met Leu Ala
705             710             715             720

Val Phe Asp Thr Asn Ile Leu Trp Val Asn Pro Asp Cys Gly Leu Lys
            725             730             735

Thr Arg Lys Tyr Thr Glu Val Lys Pro Ala Leu Thr Asn Met Val Ser
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Ala Thr Lys Leu Ile Arg Thr Gln Leu Ala Ser Ala Lys
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4

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Asp Leu Gln Lys Val Ala Ala Asp Leu Arg Ser Ser Ile Trp Lys Gln
        35                  40                  45

Met Ala Gly Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Phe Ser Phe
    50                  55                  60

Tyr Asp Gln Leu Leu Asp Ala Thr Ala Thr Leu Gly Ala Val Pro Pro
65                  70                  75                  80

Arg Tyr Gly Trp Thr Gly Gly Glu Ile Gly Phe Asp Thr Tyr Phe Ser
                85                  90                  95

Met Ala Arg Gly Asn Ala Thr Val Pro Ala Met Glu Met Thr Lys Trp
            100                 105                 110

Phe Asp Thr Asn Tyr His Phe Ile Val Pro Glu Leu Gly Pro Asp Val
            115                 120                 125

Asn Phe Thr Xaa Ala Ser Gln Lys Ala Val Asp Glu Tyr Lys Glu Ala
    130                 135                 140

Lys Ala Leu Gly Val Asp Thr Ile Pro Val Leu Val Gly Pro Val Thr
145                 150                 155                 160

Tyr Leu Leu Leu Ser Lys Pro Ala Lys Gly Val Glu Lys Ser Phe Ser
                165                 170                 175

Leu Leu Ser Leu Leu Pro Lys Val Leu Ala Val Tyr Lys Glu Val Ile
            180                 185                 190

Ala Asp Leu Lys Ala Ala Gly Ala Ser Trp Ile Gln Phe Asp Glu Pro
    195                 200                 205

Thr Leu Val Leu Asp Leu Glu Ser His Lys Leu Gln Ala Phe Thr Asp
    210                 215                 220

Ala Tyr Ala Glu Leu Ala Pro Ala Leu Ser Asp Leu Asn Val Leu Val
225                 230                 235                 240

Glu Thr Tyr Phe Ala Asp Ile Pro Ala Glu Ala Tyr Lys Thr Leu Thr
                245                 250                 255

Ser Leu Asn Gly Val Thr Ala Tyr Gly Phe Asp Leu Val Arg Gly Thr
            260                 265                 270

His Thr Leu Asp Leu Ile Lys Gly Gly Phe Pro Ser Gly Lys Tyr Leu
    275                 280                 285

Phe Ala Gly Val Val Asp Gly Arg Asn Ile Trp Ala Asn Asp Leu Ala
    290                 295                 300

Ala Ser Leu Thr Thr Leu Gln Gly Leu Glu Gly Ile Val Gly Lys Asp
305                 310                 315                 320
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6

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Lys Leu Val Val Ser Thr Ser Ser Ser Leu Leu His Thr Ala Val Asp
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Leu Val Asn Glu Thr Lys Leu Asp Asp Glu Ile Lys Ser Trp Leu Ala
            340             345                 350

Phe Ala Ala Gln Lys Ile Val Glu Val Asn Ala Leu Ala Lys Ala Leu
        355             360                 365

Ser Gly Asn Lys Asp Val Ala Phe Phe Ser Ala Asn Ala Ala Ala Gln
    370          `      375                 380

Ala Ser Arg Lys Ser Ser Pro Arg Val Thr Asn Glu Ala Val Gln Lys
385             390                 395                     400

Ala Ala Ala Ala Leu Lys Gly Ser Asp His Arg Arg Ala Thr Asn Val
            405             410                 415

Ser Ala Arg Leu Asp Ala Gln Gln Lys Lys Leu Asn Leu Pro Ile Leu
        420             425                 430

Pro Thr Thr Thr Ile Gly Ser Phe Pro Gln Thr Val Glu Leu Arg Arg
    435             440                 445

Val Arg Arg Glu Phe Lys Ala Asn Lys Ile Ser Glu Glu Glu Tyr Val
    450             455                 460

Lys Ser Ile Lys Glu Glu Ile Arg Lys Val Val Glu Leu Gln Glu Glu
465             470                 475                     480

Leu Asp Ile Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met
            485             490                 495

Val Glu Tyr Phe Gly Glu Gln Leu Ser Gly Phe Ala Phe Thr Val Asn
            500             505                 510

Gly Trp Val Gln Ser Tyr Gly Ser Arg Cys Val Lys Pro Pro Ile Ile
        515             520                 525

Tyr Gly Asp Val Ser Arg Pro Lys Pro Met Thr Val Phe Trp Ser Ser
    530             535                 540

Leu Ala Gln Ser Phe Thr Lys Arg Pro Met Lys Gly Met Leu Thr Gly
545             550                 555                     560

Pro Val Thr Ile Leu Asn Trp Ser Phe Val Arg Asn Asp Gln Pro Arg
            565             570                 575

Ser Glu Thr Thr Tyr Gln Ile Ala Leu Ala Ile Lys Asp Glu Val Glu
            580             585                 590

Asp Leu Glu Lys Ala Gly Ile Thr Val Ile Gln Ile Asp Glu Ala Ala
        595             600                 605

Leu Arg Glu Gly Leu Pro Leu Arg Lys Ser Glu Gln Ala His Tyr Leu
    610             615                 620

Asp Trp Ala Val His Ala Phe Arg Ile Thr Asn Val Gly Val Gln Asp
625             630                 635                     640
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7

Thr Thr Gln Ile His Thr His Met Cys Tyr Ser Asn Phe Asn Asp Ile
            645             650             655

Ile His Ser Ile Ile Asp Met Asp Ala Asp Val Ile Thr Ile Glu Asn
            660             665             670

Ser Arg Ser Asp Glu Lys Leu Leu Ser Val Phe Arg Glu Gly Val Lys
        675             680             685

Tyr Gly Ala Gly Ile Gly Pro Gly Val Tyr Asp Ile His Ser Pro Arg
    690             695             700

Ile Pro Pro Thr Glu Glu Ile Ala Asp Arg Ile Asn Lys Met Leu Ala
705             710             715             720

Val Leu Glu Lys Asn Ile Leu Trp Val Asn Pro Asp Cys Gly Leu Lys
            725             730             735

Thr Arg Lys Tyr Thr Glu Val Lys Pro Pro Ser Gln Asn Met Val Ala
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Ala Ala Lys Leu Ile Arg Tyr Glu Leu Ala Lys
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8

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            20                  25                  30

Asp Leu Lys Lys Val Ala Ala Asp Leu Arg Ser Ser Ile Trp Lys Gln
        35                  40                  45

Met Ala Asp Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Phe Ser Tyr
    50                  55                  60

Tyr Asp Gln Val Leu Asp Thr Thr Ala Met Leu Gly Ala Val Pro Ala
65                  70                  75                  80

Arg Tyr Asn Trp Ala Gly Gly Glu Ile Ala Phe Asp Thr Tyr Phe Ser
                85                  90                  95

Met Ala Arg Gly Asn Ala Ser Val Pro Ala Met Glu Met Thr Lys Trp
            100                 105                 110

Phe Asp Thr Asn Tyr His Phe Ile Val Pro Glu Leu Gly Pro Asp Val
        115                 120                 125

Asn Phe Ser Tyr Ala Ser His Lys Ala Val Asp Glu Tyr Lys Glu Ala
    130                 135                 140

Lys Gly Leu Gly Val Asp Thr Val Pro Val Leu Ile Gly Pro Val Ser
145                 150                 155                 160

Tyr Leu Leu Leu Ser Lys Pro Ala Lys Gly Val Glu Lys Ser Phe Pro
                165                 170                 175

Leu Leu Ser Leu Leu Asp Lys Val Leu Pro Ile Tyr Lys Glu Val Ile
            180                 185                 190

Ala Glu Leu Lys Ala Ala Gly Ala Ser Trp Ile Gln Phe Asp Glu Pro
        195                 200                 205

Thr Leu Val Leu Asp Leu Gln Ala His Gln Leu Glu Ala Phe Thr Lys
    210                 215                 220
```

9

```
Ala Tyr Ala Glu Leu Glu Ser Ser Leu Ser Gly Leu Asn Val Leu Thr
225               230               235                   240

Glu Thr Tyr Phe Ala Asp Val Pro Ala Glu Ala Phe Lys Thr Leu Thr
                245               250               255

Ala Leu Lys Gly Val Thr Ala Phe Gly Phe Asp Leu Val Arg Gly Ala
            260               265               270

Gln Thr Leu Asp Leu Ile Lys Gly Gly Phe Pro Ser Gly Lys Tyr Leu
            275               280               285

Phe Ala Gly Val Val Asp Gly Arg Asn Ile Trp Ala Asn Asp Leu Ala
    290               295               300

Ala Ser Leu Asn Leu Leu Gln Ser Leu Glu Gly Ile Val Gly Lys Asp
305               310               315               320

Lys Leu Val Val Ser Thr Ser Cys Ser Leu Leu His Thr Ala Val Asp
                325               330               335

Leu Val Asn Glu Thr Lys Leu Asp Asp Glu Ile Lys Ser Trp Leu Ala
            340               345               350

Phe Ala Ala Gln Lys Val Val Glu Val Asn Ala Leu Ala Lys Ala Leu
    355               360               365

Ala Gly His Lys Asp Glu Ala Phe Phe Ser Ala Asn Ala Thr Ala Gln
    370               375               380

Ala Ser Arg Lys Ser Ser Pro Arg Val Thr Asn Glu Ala Val Gln Lys
385               390               395               400

Ala Ala Ala Ala Leu Lys Gly Ser Asp His Arg Arg Ala Thr Asn Val
            405               410               415

Ser Ser Arg Leu Asp Ala Gln Gln Lys Lys Leu Asn Leu Pro Val Leu
            420               425               430

Pro Thr Thr Thr Ile Gly Ser Phe Pro Gln Thr Val Glu Leu Arg Arg
    435               440               445

Val Arg Arg Glu Tyr Lys Ala Lys Lys Ile Ser Glu Glu Glu Tyr Val
    450               455               460

Lys Ala Ile Lys Ala Glu Ile Lys Lys Val Val Asp Leu Gln Glu Glu
465               470               475                   480

Leu Asp Ile Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met
            485               490               495

Val Glu Tyr Phe Gly Glu Gln Leu Ser Gly Phe Ala Phe Thr Ala Asn
            500               505               510

Gly Trp Val Gln Ser Tyr Gly Ser Arg Cys Val Lys Pro Pro Ile Ile
        515               520               525

Tyr Gly Asp Val Ser Arg Pro Asn Pro Met Thr Val Phe Trp Ser Lys
    530               535               540
```

10

```
Thr Ala Gln Ser Met Thr Lys Arg Pro Met Lys Gly Met Leu Thr Gly
545             550             555             560

Pro Val Thr Ile Leu Asn Trp Ser Phe Val Arg Asn Asp Gln Pro Arg
            565             570             575

Phe Glu Thr Cys Tyr Gln Ile Ala Leu Ala Ile Lys Asp Glu Val Glu
        580             585             590

Asp Leu Glu Lys Ala Gly Ile Thr Val Ile Gln Ile Asp Glu Ala Ala
        595             600             605

Leu Arg Glu Gly Leu Pro Leu Arg Lys Ala Glu His Ala Phe Tyr Leu
    610             615             620

Asn Trp Ala Val His Ser Phe Arg Ile Thr Asn Val Gly Ile Gln Asp
625             630             635             640

Thr Thr Gln Ile His Thr His Met Cys Tyr Ser Asn Phe Asn Asp Ile
            645             650             655

Ile His Ser Ile Ile Asp Met Asp Ala Asp Val Ile Thr Ile Glu Asn
        660             665             670

Ser Arg Ser Asp Glu Lys Leu Leu Ser Val Phe Arg Glu Gly Val Lys
    675             680             685

Tyr Gly Ala Gly Ile Gly Pro Gly Val Tyr Asp Ile His Ser Pro Arg
    690             695             700

Ile Pro Ser Thr Glu Glu Ile Ala Asp Arg Val Asn Lys Met Leu Ala
705             710             715             720

Val Leu Asp Thr Asn Ile Leu Trp Val Asn Pro Asp Cys Gly Leu Lys
            725             730             735

Thr Arg Lys Tyr Ala Glu Val Lys Pro Ala Leu Glu Asn Met Val Ser
        740             745             750

Ala Ala Lys Ala Ile Arg Thr Gln Leu Ala Ser Ser Lys
        755             760             765
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<210> 7
<211> 475
<212> DNA
<213> Triticum aestivum

<220>
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<222> (344)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (367)
<223> n = A, C, G, or T

<220>
<221> unsure

11

<222> (433)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (452)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (473)..(474)
<223> n = A, C, G, or T

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cgccatcctc ctcctctccc cctatcgtct tcctccccat ctccggcgcc gctccgcgac    60
tcctccaagg aaagatggca tcccacattg ttggataccc tcgcatgggc cccaagaggg   120
agctcaagtt tgccttggag tctttctggg atgggaagag cagcgctgag gatttggaga   180
aggttgccgc cgacctcagg gccagcatct ggaagcagat gtcagaggct gggattaagt   240
acattcccag caacaccttc tcatactatg accaggtgct tgacacaacg gccatgcttg   300
gtgccgtccc ggaccgctac tcatggactg gcggagagat tggncacagc acctacttct   360
caatggncaa gggcaatgcc actgtccctg ctatggagat gaccaagtgg tttgacacca   420
actaacactt cantgtgcct gaattgagcc ancaaccaag ttctcatatg ctnna        475

<210> 8
<211> 124
<212> PRT
<213> Triticum aestivum

<220>
<221> UNSURE
<222> (98)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (117)
<223> Xaa = any amino acid

<220>
<221> UNSURE
<222> (120)
<223> Xaa = any amino acid

<400> 8
Met Ala Ser His Ile Val Gly Tyr Pro Arg Met Gly Pro Lys Arg Glu
  1               5                  10                  15

Leu Lys Phe Ala Leu Glu Ser Phe Trp Asp Gly Lys Ser Ser Ala Glu
             20                  25                  30

Asp Leu Glu Lys Val Ala Ala Asp Leu Arg Ala Ser Ile Trp Lys Gln
         35                  40                  45

Met Ser Glu Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Phe Ser Tyr
     50                  55                  60

Tyr Asp Gln Val Leu Asp Thr Thr Ala Met Leu Gly Ala Val Pro Asp
 65                  70                  75                  80

12

```
Arg Tyr Ser Trp Thr Gly Gly Glu Ile Gly His Ser Thr Tyr Phe Ser
                85                  90                  95

Met Xaa Lys Gly Asn Ala Thr Val Pro Ala Met Glu Met Thr Lys Trp
            100                 105                 110

Phe Asp Thr Asn Xaa His Phe Xaa Val Pro Glu Leu
        115                 120
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<210> 9
<211> 628
<212> DNA
<213> Triticum aestivum

<220>
<221> unsure
<222> (219)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (254)
<223> n = A, C, G, or T

<220>
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<222> (300)
<223> n = A, C, G, or T

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<222> (319)
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<220>
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<222> (331)
<223> n = A, C, G, or T

<220>
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<222> (335)
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<220>
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<220>
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<220>
<221> unsure
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<220>
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<222> (360)
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<220>
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<220>
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<222> (416)
<223> n = A, C, G, or T

<220>
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<222> (424)
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<222> (428)
<223> n = A, C, G, or T

<220>
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<222> (440)
<223> n = A, C, G, or T

<220>
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<222> (455)
<223> n = A, C, G, or T

<220>
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<222> (469)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (473)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (484)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (504)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (506)
<223> n = A, C, G, or T
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<220>
<221> unsure
<222> (526)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (533)
<223> n = A, C, G, or T

<220>
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<222> (535)
<223> n = A, C, G, or T

<220>
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<222> (552)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (568)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (580)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (598)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (600)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (606)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (613)
<223> n = A, C, G, or T

<400> 9
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ctgaccaccg ccgtgctacc cctgtctctg ctagactgga cgctcagcag aagaagctca 120
accttcctat cctcccaaca acaacaattg gttcattccc tcagacaatg gacctcagga 180
gggtccgccg tgagtacaag gcgaaagaag atctctgang aggagtatgt cagtgctatc 240
aaggaagaaa ttancaaagg ttgtcaagat tcaaagagga gcttgacatt gatgttctcn 300
tccaatggag aagcctgana aaaatgacat nggtnaanta cttcggcnan caaattatcn 360
gggtttgcaa ttactgccaa tggatgggtg caatcctatg gattacttgc gtnaancacc 420
gatnatcnat gggatgtaan cgcccaaccc atganatctt ctggtcaana tgntcaggac 480
atancctccc ccaatgaagg aatntnacgg cctttaaatc ccaacnggct ttntnagaac 540

15

```
acaaccaggt tnagaatgca caaattcnct gccataaaan gagttaggtt ccagctgngn 600
atcagngtca atnatagggg ccaaaagg                                    628
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\<210\> 10
\<211\> 118
\<212\> PRT
\<213\> Triticum aestivum

\<220\>
\<221\> UNSURE
\<222\> (8)
\<223\> Xaa = any amino acid

\<220\>
\<221\> UNSURE
\<222\> (72)..(73)
\<223\> Xaa = any amino acid

\<220\>
\<221\> UNSURE
\<222\> (84)
\<223\> Xaa = any amino acid

\<220\>
\<221\> UNSURE
\<222\> (100)
\<223\> Xaa = any amino acid

\<220\>
\<221\> UNSURE
\<222\> (106)
\<223\> Xaa = any amino acid

\<220\>
\<221\> UNSURE
\<222\> (110)
\<223\> Xaa = any amino acid

\<220\>
\<221\> UNSURE
\<222\> (112)
\<223\> Xaa = any amino acid

\<220\>
\<221\> UNSURE
\<222\> (116)
\<223\> Xaa = any amino acid

\<400\> 10
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Ser Ser Pro Arg Val Asn Asn Xaa Glu Val Gln Lys Ala Ala Ala Ala
 1               5                   10                      15

Leu Lys Gly Ser Asp His Arg Arg Ala Thr Pro Val Ser Ala Arg Leu
            20                  25                  30

Asp Ala Gln Gln Lys Lys Leu Asn Leu Pro Ile Leu Pro Thr Thr Thr
        35                  40                  45

Ile Gly Ser Phe Pro Gln Thr Met Asp Leu Arg Arg Val Arg Arg Glu
    50                  55                  60
```

Tyr Lys Ala Lys Glu Asp Leu Xaa Xaa Gly Val Cys Gln Cys Tyr Gln
65                  70              75                  80

Gly Arg Asn Xaa Gln Arg Leu Ser Arg Phe Lys Glu Glu Leu Asp Ile
              85              90                  95

Asp Val Leu Xaa Gln Trp Arg Ser Leu Xaa Lys Met Thr Xaa Val Xaa
              100             105                 110

Tyr Phe Gly Xaa Gln Ile
          115

<210> 11
<211> 765
<212> PRT
<213> Catharanthus roseus

<400> 11
Met Ala Ser His Ile Val Gly Tyr Pro Arg Met Gly Pro Lys Arg Glu
  1             5                 10                  15

Leu Lys Phe Ala Leu Glu Ser Phe Trp Asp Lys Lys Ser Ser Ala Glu
              20              25                  30

Asp Leu Gln Lys Val Ala Ala Asp Leu Arg Ser Ser Ile Trp Lys Gln
          35              40                  45

Met Ala Asp Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Phe Ser Tyr
      50                  55                  60

Tyr Asp Gln Val Leu Asp Thr Ala Thr Met Leu Gly Ala Val Pro Pro
65                  70                  75                  80

Arg Tyr Asn Phe Ala Gly Gly Glu Ile Gly Phe Asp Thr Tyr Phe Ser
              85                  90                  95

Met Ala Arg Gly Asn Ala Ser Val Pro Ala Met Glu Met Thr Lys Trp
          100             105                 110

Phe Asp Thr Asn Tyr His Tyr Ile Val Pro Glu Leu Gly Pro Glu Val
          115             120                 125

Asn Phe Ser Tyr Ala Ser His Lys Ala Val Asn Glu Tyr Lys Glu Ala
          130             135                 140

Lys Glu Leu Gly Val Asp Thr Val Pro Val Leu Val Gly Pro Val Thr
145                 150                 155                 160

Phe Leu Leu Leu Ser Lys Pro Ala Lys Gly Val Glu Lys Thr Phe Pro
              165             170                 175

Leu Leu Ser Leu Leu Asp Lys Ile Leu Pro Val Tyr Lys Glu Val Ile
              180             185                 190

Gly Glu Leu Lys Ala Ala Gly Ala Ser Trp Ile Gln Phe Asp Glu Pro
          195             200                 205

Thr Leu Val Leu Asp Leu Glu Ser His Gln Leu Glu Ala Phe Thr Lys
      210             215                 220

17

```
Ala Tyr Ser Glu Leu Glu Ser Thr Leu Ser Gly Leu Asn Val Ile Val
225             230             235             240

Glu Thr Tyr Phe Ala Asp Ile Pro Ala Glu Thr Tyr Lys Ile Leu Thr
            245             250             255

Ala Leu Lys Gly Val Thr Gly Phe Gly Phe Asp Leu Val Arg Gly Ala
            260             265             270

Lys Thr Leu Asp Leu Ile Lys Gly Gly Phe Pro Ser Gly Lys Tyr Leu
            275             280             285

Phe Ala Gly Val Val Asp Gly Arg Asn Ile Trp Ala Asn Asp Leu Ala
            290             295             300

Ala Ser Leu Ser Thr Leu Gln Ser Leu Glu Gly Ile Val Gly Lys Asp
305             310                 315             320

Lys Leu Val Val Ser Thr Ser Cys Ser Leu Leu His Thr Ala Val Asp
                325             330             335

Leu Val Asn Glu Pro Lys Leu Asp Lys Glu Ile Lys Ser Trp Leu Ala
            340             345             350

Phe Ala Ala Gln Lys Val Val Glu Val Asn Ala Leu Ala Lys Ala Leu
            355             360             365

Ala Gly Glu Lys Asp Glu Ala Phe Phe Ser Glu Asn Ala Ala Ala Gln
            370             375             380

Ala Ser Arg Lys Ser Ser Pro Arg Val Thr Asn Gln Ala Val Gln Lys
385             390             395             400

Ala Ala Ala Ala Leu Arg Gly Ser Asp His Arg Arg Ala Thr Thr Val
                405             410             415

Ser Ala Arg Leu Asp Ala Gln Gln Lys Lys Leu Asn Leu Pro Val Leu
            420             425             430

Pro Thr Thr Thr Ile Gly Ser Phe Pro Gln Thr Leu Glu Leu Arg Arg
            435             440             445

Val Arg Arg Glu Tyr Lys Ala Lys Lys Ile Ser Glu Asp Asp Tyr Val
            450             455             460

Lys Ala Ile Lys Glu Glu Ile Ser Lys Val Val Lys Leu Gln Glu Glu
465             470             475             480

Leu Asp Ile Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met
            485             490             495

Val Glu Tyr Phe Gly Glu Gln Leu Ser Gly Phe Ala Phe Thr Ala Asn
            500             505             510

Gly Trp Val Gln Ser Tyr Gly Ser Arg Cys Val Lys Pro Pro Ile Ile
            515             520             525

Tyr Gly Asp Val Ser Arg Pro Asn Pro Met Thr Val Phe Trp Ser Gln
    530             535             540
```

18

```
Thr Ala Gln Ser Met Thr Lys Arg Pro Met Lys Gly Met Leu Thr Gly
545             550             555             560

Pro Val Thr Ile Leu Asn Trp Ser Phe Val Arg Asn Asp Gln Pro Arg
            565             570             575

Phe Glu Thr Cys Tyr Gln Ile Ala Leu Ala Ile Lys Asp Glu Val Glu
            580             585             590

Asp Leu Glu Lys Ala Gly Ile Asn Val Ile Gln Ile Asp Glu Ala Ala
        595             600             605

Leu Arg Glu Gly Leu Pro Leu Arg Lys Ala Glu His Ala Phe Tyr Leu
    610             615             620

Asp Trp Ala Val His Ser Phe Arg Ile Thr Asn Leu Pro Leu Gln Asp
625             630             635             640

Thr Thr Gln Ile His Thr His Met Cys Tyr Ser Asn Phe Asn Asp Ile
            645             650             655

Ile His Ser Ile Ile Asp Met Asp Ala Asp Val Met Thr Ile Glu Asn
            660             665             670

Ser Arg Ser Ser Glu Lys Leu Leu Ser Val Phe Arg Glu Gly Val Lys
        675             680             685

Tyr Gly Ala Gly Ile Gly Pro Gly Val Tyr Asp Ile His Ser Pro Arg
    690             695             700

Ile Pro Ser Thr Glu Glu Ile Ala Asp Arg Ile Asn Lys Met Leu Ala
705             710             715             720

Val Leu Asp Thr Asn Ile Leu Trp Val Asn Pro Asp Cys Gly Leu Lys
            725             730             735

Thr Arg Lys Tyr Ala Glu Val Lys Pro Ala Leu Glu Asn Met Val Ser
            740             745             750

Ala Ala Lys Leu Ile Arg Thr Gln Leu Ala Ser Ala Lys
        755             760             765

<210> 12
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthetic oligonucleotide

<400> 12
atccaacaat gtgagatgtc atgaattctg ac                                    32

<210> 13
<211> 32
<212> DNA
<213> Artificial Sequence
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19

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<220>
<223> Description of Artificial Sequence:  Synthetic oligonucleotide

<400> 13
gtcagaattc atgacatctc acattgttgg at                                    32

<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthetic oligonucleotide

<400> 14
ctcacggtcc gatgagaagc tcct                                             24

<210> 15
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthetic oligonucleotide

<400> 15
gatcggtacc tcacttggag ctggcaagtt g                                     31

<210> 16
<211> 1638
<212> DNA
<213> Zea mays

<400> 16
gaattccggc tcgaagccgc cgcgaccgaa cgagcgaagc gtcccttccc gcgccgacgc    60
cgaaacccta gctcctctta cgccatggcc accgtgtcgc tcactccgca ggcggtcttc   120
tccaccgagt ccggcggcgc cctggcctct gccaccatcc tccgcttccc gccaaacttc   180
gtccgcctcc gcggcggcgg atgtcagcgc aattcctaac gctaaggttg cgcagccgtc   240
cgccgtcgta ttggccgagc gtaacctgct cggctccgac gccagcctcg ccgtccacgc   300
gggggagagg ctgggaagaa ggatagccac ggatgctatc accacgccgg tagtgaacac   360
gtcggcctac tggttcaaca actcgcaaga gctaatcgac tttaaggagg ggaggcatgc   420
tagcttcgag tatgggaggt atgggaaccc gaccacggag gcattagaga agaagatgag   480
cgcactggag aaagcagagt ccaccgtgtt tgtggcgtca gggatgtatg cagctgtggc   540
tatgctcagc gcacttgtcc ctgctggtgg gcacattgtg accaccacgg attgctaccg   600
caagacaagg atttacatgg aaaatgagct ccctaagagg ggaatttcga tgactgtcat   660
taggcctgct gacatggatg ctctccaaaa tgccttggac aacaataatg tatctctttt   720
cttcacggag actcctacaa atccatttct cagatgcatt gatattgaac atgtatcaaa   780
tatgtgccat agcaagggag cgttgctttg tattgacagt actttcgcgt cacctatcaa   840
tcagaaggca ttaactttag gtgctgacct agttattcat tctgcaacga agtacattgc   900
tggacacaat gatgttattg gaggatgcgt cagtggcaga gatgagttag tttccaaagt   960
tcgtatttac caccatgtag ttggtggtgt tctaaacccg aatgctgcgt accttatcct  1020
tcgaggtatg aagacactgc atctccgtgt gcaatgtcag aacgacactg ctcttcggat  1080
ggcccagttt ttagaggagc atccaaagat tgctcgtgtc tactatcctg gcttgccaag  1140
tcaccctgaa catcacattg ccaagagtca aatgactggc tttggcggtg ttgttagttt  1200
tgaggttgct ggagactttg atgctacgag gaaattcatt gattctgtta aaatacccta  1260
tcatgcgcct tcttttggag gctgtgagag cataattgat cagcctgcca tcatgtccta  1320
ctgggattca aaggagcagc gggacatcta cgggatcaag acaacctga tcaggttcag   1380
cattggtgtg gaggatttcg aggatcttaa gaacgatctc gtgcaggccc tcgagaagat  1440
ctaagcactc taatcagttt gtattgacaa aatatgaggt gatggctgtc ttggatcttg  1500
tcaagatctg tgacaatgat atgagctgat gactgcgaat aagttctctt ttgcttattt  1560
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20

tatccgtcaa attcaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1620
aaaaaaaaaa aactcgag                                                    1638

<210> 17
<211> 480
<212> PRT
<213> Zea mays

<400> 17
Asn Ser Gly Ser Lys Pro Pro Arg Pro Asn Glu Arg Ser Val Pro Ser
 1               5                   10                  15

Arg Ala Asp Ala Glu Thr Leu Ala Pro Leu Thr Pro Trp Pro Pro Cys
                20                  25                  30

Arg Ser Leu Arg Arg Arg Ser Ser Pro Pro Ser Pro Ala Ala Pro Trp
            35                  40                  45

Pro Leu Pro Pro Ser Ser Ala Ser Arg Gln Thr Ser Ser Ala Ser Ala
    50                  55                  60

Ala Ala Asp Val Ser Ala Ile Pro Asn Ala Lys Val Ala Gln Pro Ser
65                  70                  75                  80

Ala Val Val Leu Ala Glu Arg Asn Leu Leu Gly Ser Asp Ala Ser Leu
                85                  90                  95

Ala Val His Ala Gly Glu Arg Leu Gly Arg Arg Ile Ala Thr Asp Ala
            100                 105                 110

Ile Thr Thr Pro Val Val Asn Thr Ser Ala Tyr Trp Phe Asn Asn Ser
            115                 120                 125

Gln Glu Leu Ile Asp Phe Lys Glu Gly Arg His Ala Ser Phe Glu Tyr
    130                 135                 140

Gly Arg Tyr Gly Asn Pro Thr Thr Glu Ala Leu Glu Lys Lys Met Ser
145                 150                 155                 160

Ala Leu Glu Lys Ala Glu Ser Thr Val Phe Val Ala Ser Gly Met Tyr
                165                 170                 175

Ala Ala Val Ala Met Leu Ser Ala Leu Val Pro Ala Gly Gly His Ile
            180                 185                 190

Val Thr Thr Thr Asp Cys Tyr Arg Lys Thr Arg Ile Tyr Met Glu Asn
            195                 200                 205

Glu Leu Pro Lys Arg Gly Ile Ser Met Thr Val Ile Arg Pro Ala Asp
    210                 215                 220

Met Asp Ala Leu Gln Asn Ala Leu Asp Asn Asn Val Ser Leu Phe
225                 230                 235                 240

Phe Thr Glu Thr Pro Thr Asn Pro Phe Leu Arg Cys Ile Asp Ile Glu
            245                 250                 255

His Val Ser Asn Met Cys His Ser Lys Gly Ala Leu Leu Cys Ile Asp
            260                 265                 270

21

Ser Thr Phe Ala Ser Pro Ile Asn Gln Lys Ala Leu Thr Leu Gly Ala
        275                 280                 285

Asp Leu Val Ile His Ser Ala Thr Lys Tyr Ile Ala Gly His Asn Asp
        290                 295                 300

Val Ile Gly Gly Cys Val Ser Gly Arg Asp Glu Leu Val Ser Lys Val
305                 310                 315                 320

Arg Ile Tyr His His Val Val Gly Gly Val Leu Asn Pro Asn Ala Ala
        325                 330                 335

Tyr Leu Ile Leu Arg Gly Met Lys Thr Leu His Leu Arg Val Gln Cys
        340                 345                 350

Gln Asn Asp Thr Ala Leu Arg Met Ala Gln Phe Leu Glu Glu His Pro
        355                 360                 365

Lys Ile Ala Arg Val Tyr Tyr Pro Gly Leu Pro Ser His Pro Glu His
        370                 375                 380

His Ile Ala Lys Ser Gln Met Thr Gly Phe Gly Gly Val Val Ser Phe
385                 390                 395                 400

Glu Val Ala Gly Asp Phe Asp Ala Thr Arg Lys Phe Ile Asp Ser Val
                405                 410                 415

Lys Ile Pro Tyr His Ala Pro Ser Phe Gly Gly Cys Glu Ser Ile Ile
        420                 425                 430

Asp Gln Pro Ala Ile Met Ser Tyr Trp Asp Ser Lys Glu Gln Arg Asp
        435                 440                 445

Ile Tyr Gly Ile Lys Asp Asn Leu Ile Arg Phe Ser Ile Gly Val Glu
        450                 455                 460

Asp Phe Glu Asp Leu Lys Asn Asp Leu Val Gln Ala Leu Glu Lys Ile
465                 470                 475                 480

<210> 18
<211> 3639
<212> DNA
<213> Zea mays

<400> 18
tctagattac ataatacacc taataatctt gtgttgtttg tttacttctc aacttattta    60
agttggatta tattccatct tttctttttt atttgtctgt tttagttaaa aatgaactaa   120
caaacgacaa atattcgaga acgagatagt ataatctata ggataatcag acatgtcctt   180
agagggtgtt tgtttagaat tataaatatgt atagaatata taatccaaca aattttgaac   240
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gccaaaaccc tagcttctcc tactccatgg ccactgtctc gctcaccccg caggctgtct   840
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22

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<210> 19
<211> 509
<212> PRT
<213> Zea mays

<400> 19
Met Ala Thr Val Ser Leu Thr Pro Gln Ala Val Phe Ser Thr Glu Ser
 1               5                  10                  15


Gly Gly Ala Leu Ala Ser Ala Thr Ile Leu Arg Phe Pro Pro Asn Phe
            20                  25                  30

23

Val Arg Gln Leu Ser Thr Lys Ala Arg Arg Asn Cys Ser Asn Ile Gly
        35                  40                  45

Val Ala Gln Ile Val Ala Ala Ala Trp Ser Asp Cys Pro Ala Ala Arg
        50                  55                  60

Pro His Leu Gly Gly Gly Gly Arg Arg Ala Arg Gly Val Ala Ser Ser
65                  70                  75                      80

His Ala Ala Ala Ala Ser Ala Ala Ala Ala Ser Ala Ala Ala Glu
                85                  90                  95

Val Ser Ala Ile Pro Asn Ala Lys Val Ala Gln Pro Ser Ala Val Val
            100                 105                 110

Leu Ala Glu Arg Asn Leu Leu Gly Ser Asp Ala Ser Leu Ala Val His
        115                 120                 125

Ala Gly Glu Arg Leu Gly Arg Arg Ile Ala Thr Asp Ala Ile Thr Thr
    130                 135                 140

Pro Val Val Asn Thr Ser Ala Tyr Trp Phe Asn Asn Ser Gln Glu Leu
145                 150                 155                 160

Ile Asp Phe Lys Glu Gly Arg His Ala Ser Phe Glu Tyr Gly Arg Tyr
            165                 170                 175

Gly Asn Pro Thr Thr Glu Ala Leu Glu Lys Lys Met Ser Ala Leu Glu
            180                 185                 190

Lys Ala Glu Ser Thr Val Phe Val Ala Ser Gly Met Tyr Ala Ala Val
        195                 200                 205

Ala Met Leu Ser Ala Leu Val Pro Ala Gly Gly His Ile Val Thr Thr
    210                 215                 220

Thr Asp Cys Tyr Arg Lys Thr Arg Ile Tyr Met Glu Asn Glu Leu Pro
225                 230                 235                 240

Lys Arg Gly Ile Ser Met Thr Val Ile Arg Pro Ala Asp Met Asp Ala
            245                 250                 255

Leu Gln Asn Ala Leu Asp Asn Asn Val Ser Leu Phe Phe Thr Glu
            260                 265                 270

Thr Pro Thr Asn Pro Phe Leu Arg Cys Ile Asp Ile Glu His Val Ser
        275                 280                 285

Asn Met Cys His Ser Lys Gly Ala Leu Leu Cys Ile Asp Ser Thr Phe
    290                 295                 300

Ala Ser Pro Ile Asn Gln Lys Ala Leu Thr Leu Gly Ala Asp Leu Val
305                 310                 315                 320

Ile His Ser Ala Thr Lys Tyr Ile Ala Gly His Asn Asp Val Ile Gly
            325                 330                 335

Gly Cys Val Ser Gly Arg Asp Glu Leu Val Ser Lys Val Arg Ile Tyr
        340                 345                 350

24

```
His His Val Val Gly Gly Val Leu Asn Pro Asn Ala Ala Tyr Leu Ile
        355                 360             365

Leu Arg Gly Met Lys Thr Leu His Leu Arg Val Gln Cys Gln Asn Asp
        370             375             380

Thr Ala Leu Arg Met Ala Gln Phe Leu Glu Glu His Pro Lys Ile Ala
385                 390       ,             395                 400

Arg Val Tyr Tyr Pro Gly Leu Pro Ser His Pro Glu His His Ile Ala
            405             410             415

Lys Ser Gln Met Thr Gly Phe Gly Gly Val Val Ser Phe Glu Val Ala
            420             425             430

Gly Asp Phe Asp Ala Thr Arg Lys Phe Ile Asp Ser Val Lys Ile Pro
        435             440             445

Tyr His Ala Pro Ser Phe Gly Gly Cys Glu Ser Ile Ile Asp Gln Pro
    450             455             460

Ala Ile Met Ser Tyr Trp Asp Ser Lys Glu Gln Arg Asp Ile Tyr Gly
465             470             475                 480

Ile Lys Asp Asn Leu Ile Arg Phe Ser Ile Gly Val Glu Asp Phe Glu
            485             490             495

Asp Leu Lys Asn Asp Leu Val Gln Ala Leu Glu Lys Ile
        500             505
```

<210> 20
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 20
aattcatgag tgca                                                          14

<210> 21
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 21
aatttgcact catg                                                          14

<210> 22
<211> 1350
<212> DNA
<213> Escherichia coli

<400> 22
atggctgaaa ttgttgtctc caaatttggc ggtaccagcg tagctgattt tgacgccatg      60
aaccgcagcg ctgatattgt gctttctgat gccaacgtgc gtttagttgt cctctcggct     120

25

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tctgctggta tcactaatct gctggtcgct ttagctgaag gactggaacc tggcgagcga  180
ttcgaaaaac tcgacgctat ccgcaacatc cagtttgcca ttctggaacg tctgcgttac  240
ccgaacgtta tccgtgaaga gattgaacgt ctgctggaga acattactgt tctggcagaa  300
gcggcggcgc tggcaacgtc tccggcgctg acagatgagc tggtcagcca cggcgagctg  360
atgtcgaccc tgctgtttgt tgagatcctg cgcgaacgcg atgttcaggc acagtggttt  420
gatgtacgta aagtgatgcg taccaacgac cgatttggtc gtgcagagcc agatatagcc  480
gcgctggcgg aactggccgc gctgcagctg ctcccacgtc tcaatgaagg cttagtgatc  540
acccagggat ttatcggtag cgaaaataaa ggtcgtacaa cgacgcttgg ccgtggaggc  600
agcgattata cggcagcctt gctggcggag gctttacacg catctcgtgt tgatatctgg  660
accgacgtcc cgggcatcta caccaccgat ccacgcgtag tttccgcagc aaaacgcatt  720
gatgaaatcg cgtttgccga agcggcagag atggcaactt ttggtgcaaa agtactgcat  780
ccggcaacgt tgctacccgc agtacgcagc gatatcccgg tctttgtcgg ctccagcaaa  840
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gccgttggca agaggtatt cggcgtactg gaaccgttca acattcgcat gatttgttat 1260
ggcgcatcca gccataacct gtgcttcctg gtgcccggcg aagatgccga gcaggtggtg 1320
caaaaactgc atagtaattt gtttgagtaa                                  1350
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<210> 23
<211> 449
<212> PRT
<213> Escherichia coli

<400> 23
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Met Ala Glu Ile Val Val Ser Lys Phe Gly Gly Thr Ser Val Ala Asp
 1               5                  10                  15

Phe Asp Ala Met Asn Arg Ser Ala Asp Ile Val Leu Ser Asp Ala Asn
              20                  25                  30

Val Arg Leu Val Val Leu Ser Ala Ser Ala Gly Ile Thr Asn Leu Leu
          35                  40                  45

Val Ala Leu Ala Glu Gly Leu Glu Pro Gly Glu Arg Phe Glu Lys Leu
      50                  55                  60

Asp Ala Ile Arg Asn Ile Gln Phe Ala Ile Leu Glu Arg Leu Arg Tyr
 65                  70                  75                  80

Pro Asn Val Ile Arg Glu Glu Ile Glu Arg Leu Leu Glu Asn Ile Thr
                  85                  90                  95

Val Leu Ala Glu Ala Ala Ala Leu Ala Thr Ser Pro Ala Leu Thr Asp
              100                 105                 110

Glu Leu Val Ser His Gly Glu Leu Met Ser Thr Leu Leu Phe Val Glu
          115                 120                 125

Ile Leu Arg Glu Arg Asp Val Gln Ala Gln Trp Phe Asp Val Arg Lys
      130                 135                 140

Val Met Arg Thr Asn Asp Arg Phe Gly Arg Ala Glu Pro Asp Ile Ala
145                 150                 155                 160

Ala Leu Ala Glu Leu Ala Ala Leu Gln Leu Leu Pro Arg Leu Asn Glu
              165                 170                 175
```

26

```
Gly Leu Val Ile Thr Gln Gly Phe Ile Gly Ser Glu Asn Lys Gly Arg
            180                 185                 190

Thr Thr Thr Leu Gly Arg Gly Gly Ser Asp Tyr Thr Ala Ala Leu Leu
            195                 200                 205

Ala Glu Ala Leu His Ala Ser Arg Val Asp Ile Trp Thr Asp Val Pro
    210                 215                 220

Gly Ile Tyr Thr Thr Asp Pro Arg Val Val Ser Ala Ala Lys Arg Ile
225                 230                 235                 240

Asp Glu Ile Ala Phe Ala Glu Ala Ala Glu Met Ala Thr Phe Gly Ala
                245                 250                 255

Lys Val Leu His Pro Ala Thr Leu Leu Pro Ala Val Arg Ser Asp Ile
            260                 265                 270

Pro Val Phe Val Gly Ser Ser Lys Asp Pro Arg Ala Gly Gly Thr Leu
            275                 280                 285

Val Cys Asn Lys Thr Glu Asn Pro Pro Leu Phe Arg Ala Leu Ala Leu
    290                 295                 300

Arg Arg Asn Gln Thr Leu Leu Thr Leu His Ser Leu Asn Met Leu His
305                 310                 315                 320

Ser Arg Gly Phe Leu Ala Glu Val Phe Gly Ile Leu Ala Arg His Asn
            325                 330                 335

Ile Ser Val Asp Leu Ile Thr Thr Ser Glu Val Ser Val Ala Leu Thr
            340                 345                 350

Leu Asp Thr Thr Gly Ser Thr Ser Thr Gly Asp Thr Leu Leu Thr Gln
            355                 360                 365

Ser Leu Leu Met Glu Leu Ser Ala Leu Cys Arg Val Glu Val Glu Glu
    370                 375                 380

Gly Leu Ala Leu Val Ala Leu Ile Gly Asn Asp Leu Ser Lys Ala Cys
385                 390                 395                 400

Ala Val Gly Lys Glu Val Phe Gly Val Leu Glu Pro Phe Asn Ile Arg
            405                 410                 415

Met Ile Cys Tyr Gly Ala Ser Ser His Asn Leu Cys Phe Leu Val Pro
            420                 425                 430

Gly Glu Asp Ala Glu Gln Val Val Gln Lys Leu His Ser Asn Leu Phe
            435                 440                 445

Glu                                                                    (


<210> 24
<211> 36
<212> DNA
<213> Artificial Sequence
```

27

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 24
gatccatggc tgaaattgtt gtctccaaat ttggcg                          36


<210> 25
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 25
gtaccgccaa atttggagac aacaatttca gccatg                          36


<210> 26
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 26
atggcagcca agatgcttgc attgttcgct                                 30


<210> 27
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 27
gaatgcagca ccaacaaagg gttgctgtaa                                 30


<210> 28
<211> 2123
<212> DNA
<213> Zea mays

<400> 28
tctagagcct attaccatct ctactcacgg gtcgtagagg tggtgaggta ggctacagct    60
ggtgacaatc ctactcaccc tttgtaatcc tctacggctc tacgcgtagt taattggtta   120
gatgtcaacc ccctctctaa gtggcagtag tgggcttggt tatacctgct agtgcctggg   180
gatgttctat ttttctagta gtgcttgatc aaacattgca tagtttgact tgggacaaac   240
tgtctgatat atatatatat ttttgggcag agggagcagt aagaacttat ttagaaatgt   300
aatcatttgt taaaaaggt ttaattttgc tgctttcttt cgttaatgtt gttttcacat    360
tagattttct ttgtgttata tacactggat acatacaaat tcagttgcag tagtctctta   420
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gtcacattct caataaactc gtcatgtttt actaaaagta ccttttcgaa gcatcatatt   540
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ttgttgactg catgcatcta aaataggac ctagacgatc aatcgcaatc gcatatccac     720
tattctctag gaagcaaggg aatcacatcg ccatggcagc caagatgttt gcattgtttg   780
cgctcctagc tctttgtgca accgccacta gtgctaccca tatcccaggg cacttgtcac   840
cactactgat gccattggct accatgaacc catggatgca gtactgcatg aagcaacagg   900

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gggttgccaa cttgttagcg tggccgaccc tgatgctgca gcaactgttg gcctcaccgc  960
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aattttgtta ttttaattta gttgtttcac tactacattg caaccattag tatcatgcag 1920
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cggtagaagt tctctcgtac attgtcagtc atcaggtacg caccaccata cacgcttgct 2040
taaacaaaaa aacaagtgta tgtgtttgcg aagagaatta agacaggcag acacaaagct 2100
acccgacgat ggcgagtcgg tca                                         2123

<210> 29
<211> 211
<212> PRT
<213> Zea mays

<400> 29
Met Ala Ala Lys Met Phe Ala Leu Phe Ala Leu Leu Ala Leu Cys Ala
  1               5                  10                  15

Thr Ala Thr Ser Ala Thr His Ile Pro Gly His Leu Ser Pro Leu Leu
             20                  25                  30

Met Pro Leu Ala Thr Met Asn Pro Trp Met Gln Tyr Cys Met Lys Gln
         35                  40                  45

Gln Gly Val Ala Asn Leu Leu Ala Trp Pro Thr Leu Met Leu Gln Gln
     50                  55                  60

Leu Leu Ala Ser Pro Leu Gln Gln Cys Gln Met Pro Met Met Met Pro
 65                  70                  75                  80

Gly Met Met Pro Pro Met Thr Met Met Pro Met Pro Ser Met Met Pro
                 85                  90                  95

Ser Met Met Val Pro Thr Met Met Ser Pro Met Thr Met Ala Ser Met
             100                 105                 110

Met Pro Pro Met Met Met Pro Ser Met Ile Ser Pro Met Thr Met Pro
         115                 120                 125

Ser Met Met Pro Ser Met Ile Met Pro Thr Met Met Ser Pro Met Ile
         130                 135                 140

Met Pro Ser Met Met Pro Pro Met Met Met Pro Ser Met Val Ser Pro
145                 150                 155                 160

Met Met Met Pro Asn Met Met Thr Val Pro Gln Cys Tyr Ser Gly Ser
                 165                 170                 175
```

29

```
Ile Ser His Ile Ile Gln Gln Gln Gln Leu Pro Phe Met Phe Ser Pro
            180                 185                 190

Thr Ala Met Ala Ile Pro Pro Met Phe Leu Gln Gln Pro Phe Val Gly
        195                 200                 205

Ala Ala Phe
    210
```

```
<210> 30
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:   Synthetic oligonucleotide

<400> 30
atgaaccctt ggatgca                                                  17

<210> 31
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:   Synthetic oligonucleotide

<400> 31
cccacagcaa tggcgat                                                  17

<210> 32
<211> 639
<212> DNA
<213> Zea mays

<400> 32
ccatggcagc caagatgttt gcattgtttg cgctcctagc tctttgtgca accgccacta   60
gtgctaccca tatcccaggg cacttgtcac cactactgat gccattggct accatgaacc  120
cttggatgca gtactgcatg aagcaacagg gggttgccaa cttgttagcg tggccgaccc  180
tgatgctgca gcaactgttg gcctcaccgc ttcagcagtg ccagatgcca atgatgatgc  240
cgggtatgat gccaccgatg acgatgatgc cgatgccgag tatgatgcca tcgatgatgg  300
tgccgactat gatgtcacca atgacgatgg ctagtatgat gccgccgatg atgatgccaa  360
gcatgatttc accaatgacg atgccgagta tgatgccttc gatgataatg ccgaccatga  420
tgtcaccaat gattatgccg agtatgatgc caccaatgat gatgccgagc atggtgtcac  480
caatgatgat gccaaacatg atgacagtgc cacaatgtta ctctggttct atctcacaca  540
ttatacaaca acaacaatta ccattcatgt tcagccccac agcaatggcg atcccaccca  600
tgttcttaca gcagcccttt gttggtgctg cattctaga                         639

<210> 33
<211> 211
<212> PRT
<213> Zea mays

<400> 33
Met Ala Ala Lys Met Phe Ala Leu Phe Ala Leu Leu Ala Leu Cys Ala
  1               5                  10                  15
```

30

```
Thr Ala Thr Ser Ala Thr His Ile Pro Gly His Leu Ser Pro Leu Leu
            20                  25                  30

Met Pro Leu Ala Thr Met Asn Pro Trp Met Gln Tyr Cys Met Lys Gln
            35                  40              '   45

Gln Gly Val Ala Asn Leu Leu Ala Trp Pro Thr Leu Met Leu Gln Gln
        50                  55                  60

Leu Leu Ala Ser Pro Leu Gln Gln Cys Gln Met Pro Met Met Met Pro
 65                  70                  75                  80

Gly Met Met Pro Pro Met Thr Met Met Pro Met Pro Ser Met Met Pro
                85                  90                  95

Ser Met Met Val Pro Thr Met Met Ser Pro Met Thr Met Ala Ser Met
            100                 105                 110

Met Pro Pro Met Met Met Pro Ser Met Ile Ser Pro Met Thr Met Pro
        115                 120                 125

Ser Met Met Pro Ser Met Ile Met Pro Thr Met Met Ser Pro Met Ile
    130                 135                 140

Met Pro Ser Met Met Pro Pro Met Met Met Pro Ser Met Val Ser Pro
145                 150                 155                 160

Met Met Met Pro Asn Met Met Thr Val Pro Gln Cys Tyr Ser Gly Ser
                165                 170                 175

Ile Ser His Ile Ile Gln Gln Gln Gln Leu Pro Phe Met Phe Ser Pro
            180                 185                 190

Thr Ala Met Ala Ile Pro Pro Met Phe Leu Gln Gln Pro Phe Val Gly
        195                 200                 205

Ala Ala Phe
    210
```

<210> 36
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthetic oligonucleotide

<400> 36
ccacttcatg acccatatcc cagggcactt                                    30

<210> 37
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthetic oligonucleotide

<400> 37
ttctatctag aatgcagcac caacaaaggg                                    30

<210> 38
<211> 579
<212> DNA
<213> Zea mays

<400> 38
tcatgaccca tatcccaggg cacttgtcac cactactgat gccattggct accatgaacc   60
cttggatgca gtactgcatg aagcaacagg gggttgccaa cttgttagcg tggccgaccc  120
tgatgctgca gcaactgttg gcctcaccgc ttcagcagtg ccagatgcca atgatgatgc  180
cgggtatgat gccaccgatg acgatgatgc cgatgccgag tatgatgcca tcgatgatgg  240
tgccgactat gatgtcacca atgacgatgg ctagtatgat gccgccgatg atgatgccaa  300
gcatgatttc accaatgacg atgccgagta tgatgccttc gatgataatg ccgaccatga  360
tgtcaccaat gattatgccg agtatgatgc caccaatgat gatgccgagc atggtgtcac  420
caatgatgat gccaaacatg atgacagtgc cacaatgtta ctctggttct atctcacaca  480
ttatacaaca acaacaatta ccattcatgt tcagccccac agcaatggcg atcccaccca  540
tgttcttaca gcagcccttt gttggtgctg cattctaga                         579

<210> 39
<211> 191
<212> PRT
<213> Zea mays

<400> 39
Met Thr His Ile Pro Gly His Leu Ser Pro Leu Leu Met Pro Leu Ala
 1               5                  10                  15


Thr Met Asn Pro Trp Met Gln Tyr Cys Met Lys Gln Gln Gly Val Ala
            20                  25                  30


Asn Leu Leu Ala Trp Pro Thr Leu Met Leu Gln Gln Leu Leu Ala Ser
        35                  40                  45


Pro Leu Gln Gln Cys Gln Met Pro Met Met Met Pro Gly Met Met Pro
    50                  55                  60


Pro Met Thr Met Met Pro Met Pro Ser Met Met Pro Ser Met Met Val
 65                  70                  75                  80

32

```
Pro Thr Met Met Ser Pro Met Thr Met Ala Ser Met Met Pro Pro Met
                85                  90                  95

Met Met Pro Ser Met Ile Ser Pro Met Thr Met Pro Ser Met Met Pro
            100                 105                 110

Ser Met Ile Met Pro Thr Met Met Ser Pro Met Ile Met Pro Ser Met
        115                 120                 125

Met Pro Pro Met Met Met Pro Ser Met Val Ser Pro Met Met Met Pro
    130                 135                 140

Asn Met Met Thr Val Pro Gln Cys Tyr Ser Gly Ser Ile Ser His Ile
145                 150                 155                 160

Ile Gln Gln Gln Gln Leu Pro Phe Met Phe Ser Pro Thr Ala Met Ala
                165                 170                 175

Ile Pro Pro Met Phe Leu Gln Gln Pro Phe Val Gly Ala Ala Phe
            180                 185                 190
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<210> 40
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:   Synthetic oligonucleotide

<400> 40
ctagaagcct cggcaacgtc agcaacggcg gaagaatccg gtg                      43

<210> 41
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:   Synthetic oligonucleotide

<400> 41
catgcaccgg attcttccgc cgttgctgac gttgccgagg ctt                      43

<210> 42
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:   Synthetic oligonucleotide

<400> 42
gatcccatgg cgccccttaa gtccaccgcc agcctccccg tcgcccgccg ctcct         55

<210> 43
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 43
ctagaggagc ggcgggcgac ggggaggctg gcggtggact taaggggcgc catgg          55

<210> 44
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 44
catggcgccc accgtgatga tggcctcgtc ggccaccgcc gtcgctccgt tccaggggc   59

<210> 45
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 45
ttaagcccct ggaacggagc gacggcggtg gccgacgagg ccatcatcac ggtgggcgc   59

<210> 46
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 46
catggctggc ttccccacga ggaagaccaa caatgacatt acctccattg ctagcaacgg 60
tggaagagta caatg                                                   75

<210> 47
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 47
catgcattgt actcttccac cgttgctagc aatggaggta atgtcattgt tggtcttcct 60
cgtggggaag ccagc                                                   75

<210> 48
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

34

<400> 48
catggcttcc tcaatgatct cctccccagc tgttaccacc gtcaaccgtg ccggtgccgg 60
catggttgct ccattcaccg gcctcaaaag                                    90

<210> 49
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthetic oligonucleotide

<400> 49
catgcttttg aggccggtga atggagcaac catgccggca ccggcacggt tgacggtggt 60
aacagctggg gaggagatca ttgaggaagc                                    90

<210> 50
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthetic oligonucleotide

<400> 50
gactatccat ggcacattgt actcttccac c                                  31

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthetic oligonucleotide

<400> 51
tactaaccat ggcttcctca                                               20

<210> 52
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthetic oligonucleotide

<400> 52
ggccatggcc gc                                                       12

<210> 53
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthetic oligonucleotide

<400> 53
gaaaccatgg ccagtgtgat tgcgcaggca                                    30

<210> 54
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:   Synthetic oligonucleotide

<400> 54
gaaaggtacc ttacaacaac tgtgccagc                                        29

<210> 55
<211> 1494
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (1461)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (1464)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (1465)
<223> n = A, C, G, or T

<400> 55
atttgcagca caaaaagttg ttgaagtaaa tgccttggcc aaggcattgt ctggacagaa    60
ggatgaggtt ttcttttctg ctaatgctgc tgccttggct tcaaggaagt cctccccaag   120
ggtgataaat gaggctgtcc aaaaagccgc tgctgctctg aagggctctg atcatcggag   180
ggccacaaat gttagtgcca ggttggatgc tcaacagaag aaattgaatc tttctgttct   240
tccaacaact acaattggat ctttccctca aactgccgat cttagaagrg twcgycgtga   300
attcaaggct aacaagatct ccgaggaaga gtatgthaag tcaattaagg aggaaattcg   360
caaagttgtt garcttcaag aagagcttga tattgatgtt cttgttcatg gagaaccaga   420
gagaaatgat atggttgagt acttcggtga rcaattgtca ggctttgcct tcacygttaa   480
tgggtgggtg caatcctatg gttcccgttg ygtgaagcca ccratcatct atggtgatgt   540
gagccgccca aagccaatga cygtcttctg gtcatctctg gctcagagct ttaccaagcg   600
cccaatgaag ggaatgctta ccggtcctgt taccattctc aactggkcct ttgtwagaaa   660
tgaccaacct agatctgaga ccacctacca gattgctttg gctatcaagg acgaagtgga   720
ggaccttgaa aaggctggca tcactgttat ccaaattgat gaagctgctt tgagagaggg   780
tctgccactg rggaaatcag aacaagctca ctacttggac tgggctgtcc atgccttcag   840
aatcaccaat gttggtgtgc aggataccac tcagatccac acccacatgt gctactccaa   900
cttcaacgac atcatccact ccatcatcga catggacgct gatgttatca ccattgagaa   960
ctctcgctcc gatgagaagc tcctgtcagt cttccgtgaa ggtgtgaagt atggtgctgg  1020
aattgsccct ggtgtctatg acatccactc cccaagaata ccaccaactg aagaaatcgc  1080
tgacagaatc aataagatgc tggcagtgct cgagaagaac atcttgtggg tcaaccctga  1140
ctgtggtctc aagacccgca agtacactga agtgaagccc gccctcacaa acatggttgc  1200
cgcagcaaaa ctcatccgta acgaacttgc caagtgaatg gtataagaaa gtagaatcta  1260
caagttcatt ggttctgctt ttataataca ccaaagaaaa attttctata ttgggttgtt  1320
tcaataaccg tgtgtggaat atttagatgt tttagcatgc tctgtgagca attgattctt  1380
cctcaacccc tctcccctta ttttttccaa ctcctgtttt ccctaatgaa tgttgtatct  1440
ttgctttgcc gcaatcctta nttnngatat gaaatattac cagtttgtg caaa          1494

<210> 56
<211> 753
<212> PRT
<213> Escherichia coli

<400> 56
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Met Thr Ile Leu Asn His Thr Leu Gly Phe Pro Arg Val Gly Leu Arg
1               5                   10                  15

Arg Glu Leu Lys Lys Ala Gln Glu Ser Tyr Trp Ala Gly Asn Ser Thr
            20                  25                  30

Arg Glu Glu Leu Leu Ala Val Gly Arg Glu Leu Arg Ala Arg His Trp
        35                  40                  45

Asp Gln Gln Lys Gln Ala Gly Ile Asp Leu Leu Pro Val Gly Asp Phe
    50                  55                  60

Ala Trp Tyr Asp His Val Leu Thr Thr Ser Leu Leu Leu Gly Asn Val
65                  70                  75                  80

Pro Ala Arg His Gln Asn Lys Asp Gly Ser Val Asp Ile Asp Thr Leu
                85                  90                  95

Phe Arg Ile Gly Arg Gly Arg Ala Pro Thr Gly Glu Pro Ala Ala Ala
            100                 105                 110

Ala Glu Met Thr Lys Trp Phe Asn Thr Asn Tyr His Tyr Met Val Pro
            115                 120                 125

Glu Phe Val Lys Gly Gln Gln Phe Lys Leu Thr Trp Thr Gln Leu Leu
    130                 135                 140

Asp Glu Val Asp Glu Ala Leu Ala Leu Gly His Lys Val Lys Pro Val
145                 150                 155                 160

Leu Leu Gly Pro Val Thr Trp Leu Trp Leu Gly Lys Val Lys Gly Glu
                165                 170                 175

Gln Phe Asp Arg Leu Ser Leu Leu Asn Asp Ile Leu Pro Val Tyr Gln
            180                 185                 190

Gln Val Leu Ala Glu Leu Ala Lys Arg Gly Ile Glu Trp Val Gln Ile
        195                 200                 205

Asp Glu Pro Ala Leu Val Leu Glu Leu Pro Gln Ala Trp Leu Asp Ala
    210                 215                 220

Tyr Lys Pro Ala Tyr Asp Ala Leu Gln Gly Gln Val Lys Leu Leu Leu
225                 230                 235                 240

Thr Thr Tyr Phe Glu Gly Val Thr Pro Asn Leu Asp Thr Ile Thr Ala
                245                 250                 255

Leu Pro Val Gln Gly Leu His Val Asp Leu Val His Gly Lys Asp Asp
            260                 265                 270

Val Ala Glu Leu His Lys Arg Leu Pro Ser Asp Trp Leu Leu Ser Ala
            275                 280                 285
```

```
Gly Leu Ile Asn Gly Arg Asn Val Trp Arg Ala Asp Leu Thr Glu Lys
    290                 295                 300

Tyr Ala Gln Ile Lys Asp Ile Val Gly Lys Arg Asp Leu Trp Val Ala
305                 310                 315                 320

Ser Ser Cys Ser Leu Leu His Ser Pro Ile Asp Leu Ser Val Glu Thr
            325                 330                 335

Arg Leu Asp Ala Glu Val Lys Ser Trp Phe Ala Phe Ala Leu Gln Lys
            340                 345                 350

Cys His Glu Leu Ala Leu Leu Arg Asp Ala Leu Asn Ser Gly Asp Thr
            355                 360                 365

Ala Ala Leu Ala Glu Trp Ser Ala Pro Ile Gln Ala Arg Arg His Ser
    370                 375                 380

Thr Arg Val His Asn Pro Ala Val Glu Lys Arg Leu Ala Ala Ile Thr
385                 390                 395                 400

Ala Gln Asp Ser Gln Arg Ala Asn Val Tyr Glu Val Arg Ala Glu Ala
            405                 410                 415

Gln Arg Ala Arg Phe Lys Leu Pro Ala Trp Pro Thr Thr Thr Ile Gly
            420                 425                 430

Ser Phe Pro Gln Thr Thr Glu Ile Arg Thr Leu Arg Leu Asp Phe Lys
            435                 440                 445

Lys Gly Asn Leu Asp Ala Asn Asn Tyr Arg Thr Gly Ile Ala Glu His
    450                 455                 460

Ile Lys Gln Ala Ile Val Glu Gln Glu Arg Leu Gly Leu Asp Val Leu
465                 470                 475                 480

Val His Gly Glu Ala Glu Arg Asn Asp Met Val Glu Tyr Phe Gly Glu
            485                 490                 495

His Leu Asp Gly Phe Val Phe Thr Gln Asn Gly Trp Val Gln Ser Tyr
            500                 505                 510

Gly Ser Arg Cys Val Lys Pro Pro Ile Val Ile Gly Asp Ile Ser Arg
    515                 520                 525

Pro Ala Pro Ile Thr Val Glu Trp Ala Lys Tyr Ala Gln Ser Leu Thr
    530                 535                 540

Asp Lys Pro Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Cys
545                 550                 555                 560

Trp Ser Phe Pro Arg Glu Asp Val Ser Arg Glu Thr Ile Ala Lys Gln
            565                 570                 575

Ile Ala Leu Ala Cys Val Met Lys Trp Pro Ile Trp Lys Pro Leu Glu
            580                 585                 590

Leu Ala Ser Ser Arg Leu Thr Asn Arg Arg Leu Arg Gln Gly Leu Pro
            595                 600                 605
```

```
Leu Arg Arg Ser Asp Trp Asp Ala Tyr Leu Gln Trp Gly Val Glu Ala
    610             615             620

Phe Arg Ile Asn Ala Ala Val Ala Lys Asp Asp Thr Gln Ile His Thr
625             630             635             640

His Met Cys Tyr Cys Glu Phe Asn Asp Ile Met Asp Ser Ile Ala Ala
            645             650             655

Leu Asp Arg Asp Val Ile Thr Ile Glu Thr Ser Arg Ser Asp Met Glu
        660             665             670

Leu Leu Glu Ser Phe Glu Glu Phe Asp Tyr Pro Asn Glu Ile Gly Pro
        675             680             685

Gly Val Tyr Asp Ile His Ser Pro Asn Val Pro Ser Val Glu Trp Ile
    690             695             700

Glu Ala Leu Leu Lys Lys Ala Ala Lys Arg Ile Pro Ala Glu Arg Leu
705             710             715             720

Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Thr
            725             730             735

Arg Ala Ala Leu Ala Asn Met Val Gln Ala Ala Gln Asn Leu Arg Arg
            740             745             750

Gly


<210> 57
<211> 767
<212> PRT
<213> Saccharomyces cerevisiae

<400> 57
Met Val Gln Ser Ala Val Leu Gly Phe Pro Arg Ile Gly Pro Asn Arg
1               5               10              15

Glu Leu Lys Lys Ala Thr Glu Gly Tyr Trp Asn Gly Lys Ile Thr Val
            20              25              30

Asp Glu Leu Phe Lys Val Gly Lys Asp Leu Arg Thr Gln Asn Trp Lys
        35              40              45

Leu Gln Lys Glu Ala Gly Val Asp Ile Ile Pro Ser Asn Asp Phe Ser
    50              55              60

Phe Tyr Asp Gln Val Leu Asp Leu Ser Leu Leu Phe Asn Val Ile Pro
65              70              75              80

Asp Arg Tyr Thr Lys Tyr Asp Leu Ser Pro Ile Asp Thr Leu Phe Ala
            85              90              95

Met Gly Arg Gly Leu Gln Arg Lys Ala Thr Glu Thr Glu Lys Ala Val
            100             105             110

Asp Val Thr Ala Leu Glu Met Val Lys Trp Phe Asp Ser Asn Tyr His
        115             120             125
```

Tyr Val Arg Pro Thr Phe Ser Lys Thr Thr Gln Phe Lys Leu Asn Gly
    130                 135             140

Gln Lys Pro Val Asp Glu Phe Leu Glu Ala Lys Glu Leu Gly Ile His
145                 150             155                 160

Thr Arg Pro Val Leu Leu Gly Pro Val Ser Tyr Leu Phe Leu Gly Lys
                165             170             175

Ala Asp Lys Asp Ser Leu Asp Leu Glu Pro Leu Ser Leu Leu Glu Gln
            180             185                 190

Leu Leu Pro Leu Tyr Thr Glu Ile Leu Ser Lys Leu Ala Ser Ala Gly
        195             200             205

Ala Thr Glu Val Gln Ile Asp Glu Pro Val Leu Val Leu Asp Leu Pro
    210             215             220

Ala Asn Ala Gln Ala Ala Ile Lys Lys Ala Tyr Thr Tyr Phe Gly Glu
225             230             235                 240

Gln Ser Asn Leu Pro Lys Ile Thr Leu Ala Thr Tyr Phe Gly Thr Val
            245             250             255

Val Pro Asn Leu Asp Ala Ile Lys Gly Leu Pro Val Ala Ala Leu His
            260             265             270

Val Asp Phe Val Arg Ala Pro Glu Gln Phe Asp Glu Val Val Ala Ala
        275             280             285

Ile Gly Asn Lys Gln Thr Leu Ser Val Gly Ile Val Asp Gly Arg Asn
    290             295             300

Ile Trp Lys Asn Asp Phe Lys Lys Ser Ser Ala Ile Val Asn Lys Ala
305             310             315             320

Ile Glu Lys Leu Gly Ala Asp Arg Val Val Val Ala Thr Ser Ser Ser
            325             330             335

Leu Leu His Thr Pro Val Asp Leu Asn Asn Glu Thr Lys Leu Asp Ala
        340             345             350

Glu Ile Lys Gly Phe Phe Ser Phe Ala Thr Gln Lys Leu Asp Glu Val
    355             360             365

Val Val Ile Thr Lys Asn Val Ser Gly Gln Asp Val Ala Ala Ala Leu
    370             375             380

Glu Ala Asn Ala Lys Ser Val Glu Ser Arg Gly Lys Ser Lys Phe Ile
385             390             395                 400

His Asp Ala Ala Val Lys Arg Arg Val Ala Ser Ile Asp Glu Lys Met
            405             410             415

Ser Thr Arg Ala Ala Pro Phe Glu Gln Arg Leu Pro Glu Gln Gln Lys
        420             425             430

Val Phe Asn Leu Pro Leu Phe Pro Thr Thr Thr Ile Gly Ser Phe Pro
    435             440             445

40

```
Gln Thr Lys Asp Ile Arg Ile Asn Arg Asn Lys Phe Asn Lys Gly Thr
    450                 455             460

Ile Ser Ala Glu Glu Tyr Glu Lys Phe Ile Asn Ser Glu Ile Glu Lys
465                 470             475                 480

Val Ile Arg Phe Gln Glu Glu Ile Gly Leu Asp Val Leu Val His Gly
            485             490             495

Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Gly Glu Gln Ile Asn
            500             505             510

Gly Tyr Ala Phe Thr Val Asn Gly Trp Val Gln Ser Tyr Gly Ser Arg
        515             520             525

Tyr Val Arg Pro Pro Ile Ile Val Gly Asp Leu Ser Arg Pro Lys Ala
    530             535             540

Met Ser Val Lys Glu Ser Val Tyr Ala Gln Ser Ile Thr Ser Lys Pro
545             550             555                 560

Val Lys Gly Met Leu Thr Gly Pro Ile Thr Cys Leu Arg Trp Ser Phe
            565             570             575

Pro Arg Asp Asp Val Asp Gln Lys Thr Gln Ala Met Gln Leu Ala Leu
        580             585             590

Ala Leu Arg Asp Glu Val Asn Asp Leu Glu Ala Ala Gly Ile Lys Val
        595             600             605

Ile Gln Val Asp Glu Pro Ala Leu Arg Glu Gly Leu Pro Leu Arg Glu
    610             615             620

Gly Thr Glu Arg Ser Ala Tyr Tyr Thr Trp Ala Ala Glu Ala Phe Arg
625             630             635                 640

Val Ala Thr Ser Gly Val Ala Asn Lys Thr Gln Ile His Ser His Phe
            645             650             655

Cys Tyr Ser Asp Leu Asp Pro Asn His Ile Lys Ala Leu Asp Ala Asp
        660             665             670

Val Val Ser Ile Glu Phe Ser Lys Lys Asp Asp Ala Asn Tyr Ile Ala
        675             680             685

Glu Phe Lys Asn Tyr Pro Asn His Ile Gly Leu Gly Leu Phe Asp Ile
    690             695             700

His Ser Pro Arg Ile Pro Ser Lys Asp Glu Phe Ile Ala Lys Ile Ser
705             710             715                 720

Thr Ile Leu Lys Ser Tyr Pro Ala Glu Lys Phe Trp Val Asn Pro Asp
            725             730                 735

Cys Gly Leu Lys Thr Arg Gly Trp Glu Glu Thr Arg Leu Ser Leu Thr
        740             745             750

His Met Val Glu Ala Ala Lys Tyr Phe Arg Glu Gln Tyr Lys Asn
        755             760             765
```

41

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<210>   58
<211>   765
<212>   PRT
<213>   Nicotiana plumbaginifolia

<220>
<221>   UNSURE
<222>   (59)..(59)
<223>   Xaa = any amino acid

<220>
<221>   UNSURE
<222>   (102)..(102)
<223>   Xaa = any amino acid

<220>
<221>   UNSURE
<222>   (113)..(113)
<223>   Xaa = any amino acid

<220>
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<222>   (370)..(370)
<223>   Xaa = any amino acid

<220>
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<222>   (577)..(577)
<223>   Xaa = any amino acid

<220>
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<222>   (585)..(585)
<223>   Xaa = any amino acid

<220>
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<222>   (586)..(586)
<223>   Xaa = any amino acid

<220>
<221>   UNSURE
<222>   (598)..(598)
<223>   Xaa = any amino acid

<400>   58
Met Ala Ser His Ile Val Gly Tyr Pro Arg Met Gly Pro Lys Arg Glu
1               5                   10                  15

Leu Lys Phe Ala Leu Glu Ser Phe Trp Asp Gly Lys Ser Ser Ala Glu
            20                  25                  30

Asp Leu Lys Lys Val Ala Ala Asp Leu Arg Ser Ser Ile Trp Lys Gln
            35                  40                  45

Met Ala Asp Ala Gly Ile Lys Tyr Ile Pro Xaa Asn Thr Phe Ser Tyr
    50                  55                  60
```

Tyr Asp Gln Val Leu Asp Thr Thr Ala Met Leu Gly Ala Val Pro Ala
65                      70                  75                      80

Arg Tyr Asn Trp Ala Gly Gly Glu Ile Ala Phe Asp Thr Tyr Phe Ser
                85                  90                  95

Met Ala Arg Gly Asn Xaa Ser Val Pro Ala Met Glu Met Thr Lys Trp
            100                 105                 110

Xaa Asp Thr Asn Tyr His Phe Ile Val Pro Glu Leu Gly Pro Asp Val
            115                 120                 125

Asn Phe Ser Tyr Ala Ser His Lys Ala Val Asp Glu Tyr Lys Glu Ala
    130                 135                 140

Lys Gly Leu Gly Val Asp Thr Val Pro Val Leu Ile Gly Pro Val Ser
145                 150                 155                 160

Tyr Leu Leu Leu Ser Lys Pro Ala Lys Gly Val Glu Lys Ser Phe Pro
                165                 170                 175

Leu Leu Ser Leu Leu Asp Lys Val Leu Pro Ile Tyr Lys Glu Val Ile
            180                 185                 190

Ala Glu Leu Lys Ala Ala Gly Ala Ser Trp Ile Gln Phe Asp Glu Pro
        195                 200                 205

Thr Leu Val Leu Asp Leu Gln Ala His Gln Leu Glu Ala Phe Thr Lys
        210                 215                 220

Ala Tyr Ala Glu Leu Glu Ser Ser Leu Ser Gly Leu Asn Val Leu Thr
225                 230                 235                 240

Glu Thr Tyr Phe Ala Asp Val Pro Ala Glu Ala Phe Lys Thr Leu Thr
                245                 250                 255

Ala Leu Lys Gly Val Thr Ala Phe Gly Phe Asp Leu Val Arg Gly Ala
                260                 265                 270

Gln Thr Leu Asp Leu Ile Lys Gly Gly Phe Pro Ser Gly Lys Tyr Leu
        275                 280                 285

Phe Ala Gly Val Val Asp Gly Arg Asn Ile Trp Ala Asn Asp Leu Ala
    290                 295                 300

Ala Ser Leu Asn Leu Leu Gln Ser Leu Glu Gly Ile Val Gly Lys Asp
305                 310                 315                 320

Lys Leu Val Val Ser Thr Ser Cys Ser Leu Leu His Thr Ala Val Asp
                325                 330                 335

Leu Val Asn Glu Thr Lys Leu Asp Asp Glu Ile Lys Ser Trp Leu Ala
            340                 345                 350

Phe Ala Ala Gln Lys Val Val Glu Val Asn Ala Leu Ala Lys Ala Leu
    355                 360                 365

Ala Xaa His Lys Asp Glu Ala Phe Phe Ser Ala Asn Ala Thr Ala Gln
    370                 375                 380

43

```
Ala Ser Arg Lys Ser Ser Pro Arg Val Thr Asn Glu Ala Val Gln Lys
385             390             395                         400

Ala Ala Ala Ala Leu Lys Gly Ser Asp His Arg Arg Ala Thr Asn Val
            405             410                     415

Ser Ser Arg Leu Asp Ala Gln Gln Lys Lys Leu Asn Leu Pro Val Leu
            420             425                 430

Pro Thr Thr Thr Ile Gly Ser Phe Pro Gln Thr Val Glu Leu Arg Arg
        435             440             445

Val Arg Arg Glu Tyr Lys Ala Lys Lys Ile Ser Glu Glu Glu Tyr Val
    450             455             460

Lys Ala Ile Lys Ala Glu Ile Lys Lys Val Val Asp Leu Gln Glu Glu
465             470             475                         480

Leu Asp Ile Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met
            485             490         .         495

Val Glu Tyr Phe Gly Glu Gln Leu Ser Gly Phe Ala Phe Thr Ala Asn
            500             505             510

Gly Trp Val Gln Ser Tyr Gly Ser Arg Cys Val Lys Pro Pro Ile Ile
        515             520             525

Tyr Gly Asp Val Ser Arg Pro Asn Pro Met Thr Val Phe Trp Ser Lys
    530             535             540

Thr Ala Gln Ser Met Thr Lys Arg Pro Met Lys Gly Met Leu Thr Gly
545             550             555                         560

Pro Val Thr Ile Leu Asn Trp Ser Phe Val Arg Asn Asp Gln Pro Arg
            565             570                 575

Xaa Glu Thr Cys Tyr Gln Ile Ala Xaa Xaa Ile Lys Asp Glu Val Glu
            580             585             590

Asp Leu Glu Lys Ala Xaa Ile Thr Val Ile Gln Ile Asp Glu Ala Ala
    595             600             605

Leu Arg Glu Gly Leu Pro Leu Arg Lys Ala Glu His Ala Phe Tyr Leu
    610             615             620

Asn Trp Ala Val His Ser Phe Arg Ile Thr Asn Val Gly Ile Gln Asp
625             630             635                         640

Thr Thr Gln Ile His Thr His Met Cys Tyr Ser Asn Phe Asn Asp Ile
            645             650             655

Ile His Ser Ile Ile Asp Met Asp Ala Asp Val Ile Thr Ile Glu Asn
            660             665             670

Ser Arg Ser Asp Glu Lys Leu Leu Ser Val Phe Arg Glu Gly Val Lys
    675             680             685

Tyr Gly Ala Gly Ile Gly Pro Gly Val Tyr Asp Ile His Ser Pro Arg
.   690             695             700
```

44

```
Ile Pro Ser Thr Glu Glu Ile Ala Asp Arg Val Asn Lys Met Leu Ala
705                 710             715                 720

Val Leu Asp Thr Asn Ile Leu Trp Val Asn Pro Asp Cys Gly Leu Lys
                725             730             735

Thr Arg Lys Tyr Ala Glu Val Lys Pro Ala Leu Glu Asn Met Val Ser
            740             745             750

Ala Ala Lys Ala Ile Arg Thr Gln Leu Ala Ser Ser Lys
        755             760             765


<210>   59
<211>   64
<212>   PRT
<213>   Zea mays

<220>
<221>   UNSURE
<222>   (3)..(3)
<223>   Xaa = any amino acid

<220>
<221>   UNSURE
<222>   (6)..(6)
<223>   Xaa = any amino acid

<220>
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Val Thr Xaa Gly Glu Xaa Ile Ser Ala Ile Met Glu Xaa Ile Ser Lys
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Xaa Val Arg Ile Gln Glu Glu Leu Asp Ile Asp Val Val Val His Gly
            20              25                  30

Glu Pro Glu Arg Xaa Asp Xaa Xaa Xaa Tyr Phe Gly Glu Xaa Leu Ser
        35              40                  45

Ala Phe Ala Ser Thr Ala Thr Gly Trp Xaa Xaa Ser Tyr Gly Ser Arg
    50              55                  60


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<211> 411
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<213> Glycine max

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Phe Ala Ala Gln Lys Val Val Glu Val Asn Ala Leu Ala Lys Ala Leu
1               5                   10                  15

Ser Gly Gln Lys Asp Glu Val Phe Phe Ser Ala Asn Ala Ala Ala Leu
            20              25                  30

Ala Ser Arg Lys Ser Ser Pro Arg Val Ile Asn Glu Ala Val Gln Lys
        35              40                  45

Ala Ala Ala Ala Leu Lys Gly Ser Asp His Arg Arg Ala Thr Asn Val
    50              55                  60

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Ser Ala Arg Leu Asp Ala Gln Gln Lys Lys Leu Asn Leu Ser Val Leu
65                  70              75                  80

Pro Thr Thr Thr Ile Gly Ser Phe Pro Gln Thr Ala Asp Leu Arg Arg
            85              90              95

Val Arg Arg Glu Phe Lys Ala Asn Lys Ile Ser Glu Glu Glu Tyr Val
        100             105             110

Lys Ser Ile Lys Glu Glu Ile Arg Lys Val Val Glu Leu Gln Glu Glu
        115             120             125

Leu Asp Ile Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met
    130             135             140

Val Glu Tyr Phe Gly Glu Gln Leu Ser Gly Phe Ala Phe Thr Val Asn
145             150             155             160

Gly Trp Val Gln Ser Tyr Gly Ser Arg Cys Val Lys Pro Pro Ile Ile
            165             170             175

Tyr Gly Asp Val Ser Arg Pro Lys Pro Met Thr Val Phe Trp Ser Ser
        180             185             190

Leu Ala Gln Ser Phe Thr Lys Arg Pro Met Lys Gly Met Leu Thr Gly
    195             200             205

Pro Val Thr Ile Leu Asn Trp Xaa Phe Val Arg Asn Asp Gln Pro Arg
    210             215             220

Ser Glu Thr Thr Tyr Gln Ile Ala Leu Ala Ile Lys Asp Glu Val Glu
225             230             235             240

Asp Leu Glu Lys Ala Gly Ile Thr Val Ile Gln Ile Asp Glu Ala Ala
            245             250             255

Leu Arg Glu Gly Leu Pro Leu Xaa Lys Ser Glu Gln Ala His Tyr Leu
            260             265             270

Asp Trp Ala Val His Ala Phe Arg Ile Thr Asn Val Gly Val Gln Asp
        275             280             285

Thr Thr Gln Ile His Thr His Met Cys Tyr Ser Asn Phe Asn Asp Ile
    290             295             300

Ile His Ser Ile Ile Asp Met Asp Ala Asp Val Ile Thr Ile Glu Asn
305             310             315             320

Ser Arg Ser Asp Glu Lys Leu Leu Ser Val Phe Arg Glu Gly Val Lys
            325             330             335

Tyr Gly Ala Gly Ile Xaa Pro Gly Val Tyr Asp Ile His Ser Pro Arg
        340             345             350

Ile Pro Pro Thr Glu Glu Ile Ala Asp Arg Ile Asn Lys Met Leu Ala
    355             360             365

Val Leu Glu Lys Asn Ile Leu Trp Val Asn Pro Asp Cys Gly Leu Lys
    370             375             380

47

Thr Arg Lys Tyr Thr Glu Val Lys Pro Ala Leu Thr Asn Met Val Ala
385                 390             395                 400

Ala Ala Lys Leu Ile Arg Asn Glu Leu Ala Lys
            405                 410